What is Claimed is:

1. A method for identifying and/or quantifying an organism or part of an organism by a detecting its nucleotide sequence among at least 4 other homologous sequences comprising:

a. extracting original nucleotide sequences from the organism;

b. amplifying or copying with a unique pair of primers, at least part of original nucleotide sequences into target nucleotide sequences to be detected;

c. labelling said target nucleotide sequences;

d. putting into contact the labelled target nucleotide sequences with single stranded capture nucleotide sequences bound by a single predetermined link to an insoluble solid support, preferably a non porous solid support,

e. discriminating the binding of a target nucleotide sequence specific of an organism or part of it by detecting, quantifying and/or recording a signal resulting from a hybridization by complementary base pairing between the target nucleotide sequence and its corresponding capture nucleotide sequence,

wherein said capture nucleotide sequence being bound to the insoluble solid support at a specific location according to an array, said array having a density of at least 4 different bound single stranded capture nucleotide sequences/cm^2 of solid support surface and

wherein the binding between the target nucleotide sequence and its corresponding capture nucleotide sequence forms results in said signal at the expected location, the detection of a single signal allowing a discrimination of the target nucleotide sequence specific of an organism or part of it from homologous nucleotide sequences.

2. The method according to claim 1, wherein the amplified homologous original nucleotide sequence is a DNA nucleotide sequence.

3. The identification method according to claim 1, wherein the amplification is obtained by PCR with the same primer pair.

4. The method according to claim 1, wherein the amplified homologous original nucleotide sequences are mRNA first retrotranscribed into cDNA with the same primer pair.

5. The method according to claim 1, wherein the copy of the homologous original nucleotide sequences is made with the same primer pair.

6. The method according to claim 1, wherein the same capture nucleotide sequences specific for one organism are present at different locations upon the array of the solid support.

7. The method according to claim 1, wherein the specific sequence of the capture nucleotide sequence, able to hybridize with their corresponding target nucleotide sequence, is separate from the surface of the solid support by a spacer having at least 6.8 nm.

8. The method according to the claim 7, wherein said spacer is a sequence of between about 15 and about 40 bases.

9. The method according to claim 1, wherein the density of the capture nucleotide sequence bound to the surface at a specific location is superior to 10 fmoles and preferably 100 fmoles per cm^2 of solid support surface.

10. The method according to claim 1, wherein the target nucleotide sequence to be detected presents an homology with other homologous nucleotide sequences higher than 30%, preferably higher than 60%, more preferably higher than 80%.

11. The method according to claim 1, characterised in that the quantification of the organism

present in the biological sample is obtained by the quantification of the signal.

12. The method according to claim 1, characterised in that other primers are present in the amplification step for the amplification of other nucleotide sequences, such as an antibiotic resistance determining sequence.

13. The method according to claim 1, characterised in that the insoluble solid support is selected from the group consisting of glasses, electronic devices, silicon supports, plastic supports, compact discs, filters, gel layers, metallic supports or a mixture thereof.

14. The method according to claim 1, wherein the original nucleotide sequences to be detected and/or be quantified are RNA sequences submitted to a retro-transcription of the 3' or 5' end by using consensus primer and possibly a stopper sequence.

15. The method according to claim 1, wherein the original nucleotide sequences to be identified and/or quantified in a sample are *FemA* genetic sequences of Staphylococci species selected from the group consisting of S. *aureus*, S. *epidermidis*, S. *saprophyticus*, S. *hominis* and/or S. *haemolyticus*.

16. The method according to claim 1, wherein the solid support bears capture nucleotide sequences specific of the homologous sequences specific for the binding with the homologous target nucleotide sequence together with a consensus sequence for a common detection.

17. The method according to claim 1, wherein the solid support bears capture nucleotide sequences specific for the identification of two or more staphylococcus species together with a consensus sequence for a *Staplylococcus* genus identification.

18. The method according to claim 1, wherein the original sequence to be identified and/or quantified in the sample belongs to the MAGE gene family.

19. The method according to claim 1, wherein the original sequence to be identified and/or quantified in the sample belongs to the *HLA-A* genes family.

20. The method according to claim 1, wherein the original sequence to be identified and/or quantified in the sample belongs to the dopamine receptors coupled to the protein G genes family.

21. The method according to claim 1, wherein the original sequence to be identified and/or quantified in the sample belongs to the choline receptors coupled to the protein G genes family.

22. The method according to claim 1, wherein the original sequence to be detected and/or quantified in the sample belongs to the histamine receptors coupled to the protein G genes family.

23. The method according to claim 1, wherein the original sequence to be detected and/or quantified in the sample belongs the cytochrome P450 forms family.

24. A diagnostic and/or quantification kit which comprises an insoluble solid support upon which single stranded capture nucleotide sequences are bound, said single stranded capture nucleotide sequences containing a sequence of between about 10 and about 60 bases specific for a target nucleotide sequence to be detected and/or quantified and having a total length comprised between about 30 and about 600 bases, said single stranded capture nucleotide sequences being disposed upon the surface of the solid support according to an array with a density of at least 4 single stranded capture nucleotide sequences/cm^2 of the solid support surface.

25. The diagnostic kit according to claim 24, wherein the insoluble solid support is selected from the group consisting of glasses, electronic devices, silicon supports, plastic supports, compact discs, gel layers, metallic supports or a mixture thereof.

26. The diagnostic kit according to claim 24, wherein the capture nucleotide sequences are specific to a target nucleotide sequence to be detected and/or quantified which is specific for a gene selected from the group consisting of *Staphylococcus* species genes, MAGE genes family, HLA-genes family, dopamine, choline or histamine receptors coupled to the protein G genes family, cytochrome P450 forms family or GMO plants family.

27. The diagnostic kit according to claim 24, comprising biochips, for identification and/or quantification of 5 bacteria species obtained after amplification of one of their DNA sequences with one consensus primer(s) and detection on an array.

28. The diagnostic kit according to claim 24, comprising biochips, for identification and/or quantification of bacteria species together with the identification of the bacterial genus obtained after copying and/or amplification of one of their DNA or RNA sequences with one consensus primer(s) and detection on an array.

29. The diagnostic kit according to claim 24, comprising biochips, for detection and/or quantification of 15 Staplylococcus species obtained after copying and/or amplification of one of their DNA sequences with one consensus primer(s) and detection on an array.

30. The diagnostic kit according to claim 24, comprising biochips, for detection and/or quantification of 3 or more MAGE genes obtained after copying and/or amplification of one of their DNA or mRNA sequences with one consensus primer(s) and detection on an array.

31. The diagnostic kit according to claim 24, comprising biochips, for detection and/or quantification of 3 or more HLA-A sequences obtained after copying and/or amplification of one of their mRNA or DNA sequences with one consensus primer(s) and detection on an array.

32. The diagnostic kit according claim 24, comprising biochips, for detection and/or quantification of 3 or more gene sequences of receptors coupled to the protein G obtained after copying and/or amplification of one of their mRNA or DNA sequences with one consensus primer(s) and detection on an array.

33. The diagnostic kit according to claim 32, comprising biochips, for detection and/or quantification of 3 or more gene sequences of dopamine receptors coupled to the protein G obtained after copying and/or amplification of one of their mRNA or DNA sequences with one consensus primer(s) and detection on an array.

34. The diagnostic kit according to claim 32, comprising biochips, for detection and/or quantification of 3 or more gene sequences of serotonine receptors coupled to the protein G obtained after copying and/or amplification of one of their mRNA or DNA sequences with one consensus primer(s) and detection on an array.

35. The diagnostic kit according to claim 32, comprising biochips, for detection and/or quantification of 3 or more gene sequences of histamine receptors coupled to the protein G obtained after copying and/or amplification of one of their mRNA or DNA sequences with one consensus primer(s) and detection on an array.

36. The diagnostic kit according to claim 24, comprising biochips, for detection and/or quantification of 3 or more gene sequences of GMO plants obtained after copying and/or amplification of one of their mRNA or DNA sequences with one consensus primer(s) and detection on an array.

37. The diagnostic kit according to claim 24, comprising biochips, for detection and/or quantification of 3 or more gene sequences the cytochrome P450 forms obtained after copying and/or amplification of one of their mRNA or DNA sequences with one consensus primer(s) and detection on an array.

38. The method of Claim 1, wherein said organism is a microorganism.

39. The method of Claim 1, wherein said organism is present in a biological sample.